

<110> OOKURA, TETUYA KASUMI, TAKAFUMI

ASABA, EIJI

<120> ERYTHROSE REDUCTASE, ITS cDNA AND CELL WHICH THE cDNA EXPRESS

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<151> 2001-03-08

<150> JP 2001-001294

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agt Ser	gtc Val	aag Lys 35	aac Asn	gct Ala	gtc Val	aag Lys	gct Ala 40	ggg Gly	tac Tyr	cgt Arg	cat His	ttg Leu 45	gat Asp	ttg Leu	gcc Ala	144
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gta Val	tgg Trp	aat Asn	aac Asn	cgt Arg 85	cat His	gct Ala	cct Pro	gaa Glu	cat His 90	gtt Val	gag Glu	cct Pro	gca Ala	ttg Leu 95	gac Asp	288
gaa Glu	aca Thr	ttg Leu	aaa Lys 100	gaa Glu	ctt Leu	gga Gly	ttg Leu	tcc Ser 105	tac Tyr	ttg Leu	gat Asp	ttg Leu	tac Tyr 110	ttg Leu	att Ile	336
cat His	tgg Trp	ccc Pro 115	gtt Val	gcg Ala	ttc Phe	aag Lys	ttt Phe 120	act Thr	acg Thr	cct Pro	caa Gln	gaa Glu 125	cta Leu	ttc Phe	cct Pro	384
act Thr	gag Glu 130	ccg Pro	gat Asp	aac Asn	aag Lys	gaa Glu 135	ttg Leu	gcc Ala	gcg Ala	att Ile	gat Asp 140	gat Asp	tca Ser	atc Ile	aag Lys	432
ttg Leu 145	gta Val	gac Asp	act Thr	tgg Trp	aag Lys 150	gca Ala	gtt Val	gta Val	gca Ala	ctc Leu 155	aaa Lys	aaa Lys	acg Thr	ggt Gly	aag Lys 160	480

	aaa Lys															528
	gaa Glu															576
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	att Ile 210															672
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	aat Asn															768
	tac Tyr															816
	tat Tyr															864
	ttg Leu 290															912
tat Tyr 305	aaa Lys	cct Pro	tca Ser	tgg Trp	ccc Pro 310	atc Ile	agt Ser	gtg Val	ttt Phe	ggt Gly 315	aca Thr	tcg Ser	gat Asp	gaa Glu	gct Ala 320	960
	gct Ala									tga	gtto	agtt	tg g	ggaac	ctattt	1013
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Lys Val Tyr Gln Asn Gln Ser Glu Ile Gly Val Ala Leu Gln Glu Leu 50 55 60

Phe Asp Gln Gly Ile Val Lys Arg Glu Asp Leu Phe Ile Thr Ser Lys 70 75 80

Val Trp Asn Asn Arg His Ala Pro Glu His Val Glu Pro Ala Leu Asp 85 90 95

Glu Thr Leu Lys Glu Leu Gly Leu Ser Tyr Leu Asp Leu Tyr Leu Ile 100 105 110

His Trp Pro Val Ala Phe Lys Phe Thr Thr Pro Gln Glu Leu Phe Pro 115 120 125

Thr Glu Pro Asp Asn Lys Glu Leu Ala Ala Ile Asp Asp Ser Ile Lys 130 135 140

Leu Val Asp Thr Trp Lys Ala Val Val Ala Leu Lys Lys Thr Gly Lys 145 150 155 160

Thr Lys Ser Val Gly Val Ser Asn Phe Thr Thr Asp Leu Val Asp Leu 165 170 175

Val Glu Lys Ala Ser Gly Glu Arg Pro Ala Val Asn Gln Ile Glu Ala 180 185 190

His Pro Leu Leu Gln Gln Asp Glu Leu Val Ala His His Lys Ser Lys 195 200 205

Asn Ile Val Ile Thr Ala Tyr Ser Pro Leu Gly Asn Asn Val Ser Gly 210 220

Lys Pro Pro Leu Thr Gln Asn Pro Gly Ile Glu Ala Thr Ala Lys Arg 225 230 235 240

Leu Asn His Thr Pro Ala Ala Val Leu Leu Ala Trp Gly Ile Gln Arg 245 250 255

Gly Tyr Ser Val Leu Val Lys Ser Val Thr Pro Ser Arg Ile Glu Ser 260 265 270

Asn Tyr Asp Gln Ile Thr Leu Ser Pro Glu Glu Phe Gln Lys Val Thr 275 280 285

Asp Leu Ile Lys Glu Tyr Gly Glu Ser Arg Asn Asn Ile Pro Leu Asn 290 295 300

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ctt tg Leu Tr								288
gag ac Glu Th								336
cac tg His Tr								384
gct ga Ala As 13	p Pro							432
ttg tc Leu Se 145								480
acc aa Thr Ly								528

											aac Asn					576
cac His	ccc Pro	ttg Leu 195	ttg Leu	caa Gln	caa Gln	gac Asp	gag Glu 200	ttg Leu	gtt Val	gct Ala	cac His	cat His 205	aag Lys	agc Ser	aag Lys	624
aac Asn	att Ile 210	gtc Val	atc Ile	act Thr	gct Ala	tac Tyr 215	agt Ser	ccc Pro	ttg Leu	ggc Gly	aac Asn 220	aat Asn	gtc Val	gct Ala	ggt Gly	672
aaa Lys 225	cca Pro	cct Pro	ctg Leu	act Thr	gag Glu 230	aat Asn	ccc Pro	ggt Gly	att Ile	gtg Val 235	gat Asp	gct Ala	gct Ala	aag Lys	cgt Arg 240	720
ctg Leu	aac Asn	cat His	act Thr	cct Pro 245	gct Ala	gct Ala	gtg Val	ctc Leu	att Ile 250	gct Ala	tgg Trp	ggt Gly	att Ile	caa Gln 255	cgc Arg	768
											tca Ser					816
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aac Asn	ctc Leu 290	atc Ile	aag Lys	gag Glu	tac Tyr	ggt Gly 295	gag Glu	agc Ser	cgt Arg	aac Asn	aac Asn 300	gtt Val	cct Pro	ttc Phe	aac Asn	912
tac Tyr 305	aag Lys	cct Pro	tcg Ser	tgg Trp	tct Ser 310	att Ile	gac Asp	gtc Val	ttt Phe	ggt Gly 315	acc Thr	cag Gln	tac Tyr	gag Glu	gct Ala 320	960
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Gly Val Lys Leu Ala Val Lys Ala Gly Tyr Arg His Leu Asp Leu Ala 35 40 45

Lys Val Tyr Gln Asn Gln Thr Glu Ile Gly Gln Ala Leu Lys Glu Leu 50 55 60

Phe Asp Glu Gly Val Val Lys Arg Glu Asp Leu Phe Ile Thr Ser Lys 70 75 80

Leu Trp Asn Asn Arg His Ala Pro Glu His Val Glu Pro Ala Leu Asp 85 90 95

Glu Thr Leu Lys Glu Leu Gly Leu Ser Tyr Leu Asp Leu Tyr Leu Ile 100 105 110

His Trp Pro Val Ala Phe Lys Phe Thr Thr Pro Asp Glu Leu Leu Pro 115 120 125

Ala Asp Pro Thr Asn Lys Asp Leu Ala Tyr Ile Asp Asp Ser Val Lys 130 135 140

Leu Ser Asp Thr Trp Lys Ala Val Val Ala Leu Lys Lys Thr Gly Lys 145 150 155 160

Thr Lys Ser Val Gly Val Ser Asn Phe Ser Thr Arg Leu Val Asp Leu 165 170 175

Val Glu Glu Ala Ser Gly Glu Arg Pro Ala Val Asn Gln Ile Glu Ala 180 185 190 His Pro Leu Leu Gln Gln Asp Glu Leu Val Ala His His Lys Ser Lys 195 200 205

Asn Ile Val Ile Thr Ala Tyr Ser Pro Leu Gly Asn Asn Val Ala Gly 210 215 220

Lys Pro Pro Leu Thr Glu Asn Pro Gly Ile Val Asp Ala Ala Lys Arg 225 230 235 240

Leu Asn His Thr Pro Ala Ala Val Leu Ile Ala Trp Gly Ile Gln Arg 245 250 255

Gly Tyr Ser Val Leu Val Lys Ser Val Thr Pro Ser Arg Ile Lys Ser 260 265 270

Asn Phe Glu Gln Ile Thr Leu Ser Asp Glu Glu Phe Gln Arg Val Thr 275 280 285

Asn Leu Ile Lys Glu Tyr Gly Glu Ser Arg Asn Asn Val Pro Phe Asn 290 295 300

Tyr Lys Pro Ser Trp Ser Ile Asp Val Phe Gly Thr Gln Tyr Glu Ala 305 310 315 320

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					acc Thr 55										192
					aag Lys										240
					gct Ala										288
					ggt Gly										336
cac His					aag Lys										384
gct Ala	_			_	_		_		_	_	_	_	-		432
ttg Leu 145															480
acc Thr															528
gtt Val															576

cac His	ccc Pro	ttg Leu 195	ttg Leu	caa Gln	caa Gln	gac Asp	gag Glu 200	ttg Leu	gtt Val	gct Ala	cac His	cat His 205	aag Lys	agc Ser	aag Lys	624
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cgtt	tgaa	.cc t	gtaa	tgtg	rt ga	atgt	tato	ctc	attg	ttg	cato	gtct	ca t	caaa	aaaaa	1067
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Asn Ile Val Ile Thr Ala Tyr Ser Pro Leu Gly Asn Asn Val Ala Gly 210 215 220

Lys Pro Pro Leu Thr Glu Asn Pro Gly Ile Val Asp Ala Ala Lys Arg 225 230 235 240

Leu Asn His Thr Pro Ala Ala Val Leu Ile Ala Trp Gly Ile Gln Arg 245 250 255

Gly Tyr Ser Val Leu Val Lys Ser Val Thr Pro Ser Arg Ile Lys Ser 260 265 270

Asn Phe Glu Gln Ile Thr Leu Ser Asp Glu Glu Phe Gln Arg Val Thr 275 280 285

Asn Leu Ile Lys Glu Tyr Gly Glu Ser Arg Asn Asn Val Pro Phe Asn 290 295 300

Tyr Lys Pro Ser Trp Ser Ile Asp Val Phe Gly Thr Gln Asp Glu Ala 305 310 315 320

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